BioGraph User Manual

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1 Introduction

This manual assumes that you, the user, are comfortable with SBML and graphs. If this is not the case, there are numerous introductions that can be found online to bring you up to speed. The application has an intuitive interface with help where necessary so this manual simply describes the features and notes any intricacies.

The application is made up of three panes. The leftmost pane contains the actions the user can take to interact the with the application and will be referred to as the action pane. The center pane will be referred to as the container and contains the visualisation. The rightmost pane contains the properties of the most recently selected node and will be referred to as the inspector.

Actions have been grouped into sets that each have their own heading. Clicking on a heading will expand it to reveal the actions within that heading.

2 Visualisation

Once the application is loaded, it will automatically load models and visualise them. If no graphs are visible, there are likely no models in the database. The visualise models button can be clicked to reload models and visualise them again at any time. It will often be executed automatically after actions have changed information.

3 Uploading

These actions assist in adding SBML files. A schema is required to convert an SBML file into the necessary form, so one is provided by default. This schema can be changed to any valid schema using the upload schema button. Any valid SBML file can be uploaded using the upload model file. An invalid SBML file will not result in a change. Multiple SBML files can be added to the database at the same time, although this can take a long time depending on the size of the files.

4 Deletion

The clear models button allows all information to be deleted leading to a full reset.

5 Queries

Three queries are possible: querying by model name, querying by node and an arbitrary query. All of these queries are read-only however, they cannot alter information, only display it. Querying by model name allows you to enter the name of a model and view all nodes that are a part of it. Querying by node allows you to give (possibly incomplete) information about a node and view all the models that have nodes that fit this data. Some information is required however. Finally, for those users that know Cypher, an arbitrary query is allowed.

6 Merging

The start merge button allows nodes to be selected by clicking on them. A node that is selected will have a larger white outline than other nodes. You can click a node a second time to deselect it. From now on, the reset button can be clicked to reset the visualisation and cancel any effects. Once at least two nodes have been selected, the preview merge button can be clicked to view the node that all the nodes would be combined into as well as all the nodes that would then be directly connected to this new node. If this is an acceptable change, the accept merge button can be clicked to confirm the choice and reload the models with the new information in place.

7 Visualisation Container and Inspector

All nodes can be clicked to view their properties in the inspector, with the name of the property before the colon, and the value after. Nodes can be dragged to move them around and the whole visualisation can be panned and zoomed by dragging a point with the mouse and scrolling. The colour of each node is determined by its label, so nodes of the same colour are of the same type.